



DR WPI; 2000-303369/26.  
 DR N-PSDB; AAZ24881.  
 PT Novel proteins and polynucleotides representing contortrostatin useful  
 for inhibiting platelet aggregation, tumor metastasis and growth.  
 XX PS Claim 3d; FIG 3A-C; 81pp; English.  
 XX The present sequence is that of the Southern copperhead snake venom  
 disintegrin, contortrostatin, a protein that inhibits the interactions  
 between integrins and their receptors. The sequence was deduced from  
 CC isolated snake venom cDNA (see AAZ24881). The contortrostatin precursor  
 protein includes a pro-protein region, a metalloproteinase region which  
 includes a metal-binding motif, and a disintegrin region which includes  
 an RGD loop that acts as an integrin antagonist. Polypeptides comprising  
 CC the pro-region, the metalloproteinase region, and the contortrostatin  
 monomer, as well as the full-length precursor protein, can be obtained  
 CC using recombinant DNA methods. The purified proteins are used in  
 CC pharmaceutical compositions for treating diseases associated with an  
 CC integrin binding to an integrin receptor, especially to inhibit platelet  
 CC aggregation, tumor metastasis, angiogenesis, neovascularization, cell  
 CC adhesion, invasiveness, or growth (all claimed). The proteins are also  
 CC useful for treating a thrombotic disorder, e.g. preventing arterial,  
 CC venous, and microvascular thrombosis and thromboembolism, stroke,  
 CC embolism, aneurism, angina and myocardial infarction.  
 XX Revised record issued on 26-AUG-2004 : Correction to feature table key  
 CC Sequence 483 AA:  
 CC Query Match 100 %; Score 382; DB 3; Length 483;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-29; Mismatches 0; Indels 0; Gaps 0;  
 CC Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC QY 1 DAPANCCDAATCKLTGSGCAGDGLCDQCKFMKEGTVCRRARGDDDDYCNNGISAGCPR 60  
 CC DB 419 DAPANPCDAATCKLTGSGCAGDGLCDQCKFMKEGTVCRRARGDDDDYCNNGISAGCPR 478  
 CC QY 61 NPFHA 65  
 CC DB 479 NPFHA 483  
 RESULT 2  
 AAE03036  
 ID AAE03036 standard; protein; 483 AA.  
 XX  
 AC AAE03036;  
 DT 04-AUG-2001 (first entry)  
 DE Agkistrodon contortrix contortrostatin (CN) protein.  
 XX Southern copper head snake; contortrostatin; CN; cytotrophic; osteopathic;  
 KW vulnary; disintegrin; platelet aggregation; neovascularization; tumour;  
 KW integrin; angiogenesis; metastasis; invasiveness; growth; metastasis;  
 KW melanoma; carcinoma; sarcoma; therapy; thrombotic disease; osteoporosis;  
 KW wound healing.  
 XX Agkistrodon contortrix.  
 XX  
 FH Key Location/Qualifiers  
 FT 1. :190  
 FT Domain /label= Proprotein  
 FT 191 :410  
 FT  
 FT Binding-site /label= Metalloproteinase  
 FT 334 :344  
 FT /label= Zinc-binding\_motif  
 FT 419 :483  
 FT Domain /label= Disintegrin  
 FT 424 :433  
 FT Region /label= Conserved\_Sequence  
 PT /note= "This sequence is used for designing PCR primers  
 PT PCR-1 and PCR-2"  
 PT Domain 461 :463  
 PT /label= RGD\_sequence  
 XX DN WO200141791-A1.  
 XX PD 14-JUN-2001.  
 XX PR 09-DEC-2000; 2000WO-US013367.  
 XX PR 10-DEC-1999; 99US-0040295.  
 PR 08-JUN-2000; 2000US-00591552.  
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PI Markland FS, Zhou Q;  
 XX BS WPI; 2001-381494/40.  
 XX DR N-PSDB; AAD07386.  
 PT Homodimeric disintegrin useful for modulating the adhesion, motility, and  
 PT invasiveness of integrin expressing tumor cells.  
 XX Claim 12; Fig 3; 101pp; English.  
 CC The present sequence is contortrostatin (CN) protein from southern copper  
 CC head snake, CN, a homodimeric disintegrin binds to integrin  $\alpha$ v $\beta$ 2 and  
 CC induces  $\alpha$ v $\beta$ 3-mediated tyrosine phosphorylation of cHS and PAK  
 CC in tumour cells. CN is useful for modulating the adhesion, motility, and  
 CC invasiveness of integrin expressing cells, preferably tumour cells and  
 CC for inhibiting the adhesion of integrin expressing cells to virionectin.  
 CC The pharmaceutical composition comprising CN is useful for inhibiting  
 CC platelet aggregation, neovascularisation, angiogenesis, tumour  
 CC metastasis, invasiveness or growth, for inhibiting metastasis in  
 CC melanoma, carcinoma and sarcoma patients. It is also useful for treating  
 CC thrombotic diseases, osteoporosis, and wound healing in mammals  
 XX Sequence 483 AA:  
 CC Query Match 100.0%; Score 382; DB 4; Length 483;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-29; Mismatches 0; Indels 0; Gaps 0;  
 CC Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC QY 1 DAPANCCDAATCKLTGSGCAGDGLCDQCKFMKEGTVCRRARGDDDDYCNNGISAGCPR 60  
 CC DB 419 DAPANPCDAATCKLTGSGCAGDGLCDQCKFMKEGTVCRRARGDDDDYCNNGISAGCPR 478  
 CC QY 61 NPFHA 65  
 CC DB 479 NPFHA 483  
 RESULT 3  
 AAW14083  
 ID AAW14083 standard; peptide; 73 AA.  
 XX  
 AC AAW14083;  
 XX DT 17-OCT-2003 (revised)  
 DT 27-OCT-1997 (first entry)  
 XX DE Platelet aggregation inhibitor, Salmonin.  
 XX  
 KW Salmonin; inhibit; blood; platelet aggregation; venom; Korean; thrombosis.  
 KW Salmona viper; Agkistrodon halys brevicaudus; treatment; thrombosis.  
 KW Glwydius halys brevicaudus.  
 OS  
 XX FR2736266-A1.  
 FN  
 XX PD 10-JAN-1997.  
 XX



XX  
 PS Example 5; Page 38-39; 41pp; English.  
 XX  
 CC The invention relates to a cDNA encoding Saxatilin protein derived from  
 CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful  
 CC for as an anti-tumour agent and for effectively suppressing platelet  
 CC aggregation which makes it possible as and an active ingredient of anti-  
 CC platelet agent. Saxatilin is useful for inhibiting angiogenesis induced  
 CC by tumour and for inhibiting tumour without cytotoxicity. The present  
 CC sequence is Agkistrodon saxatilis emelianov saxatilin protein. (Updated  
 CC on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 73 AA;  
 Query Match 90.6%; Score 346; DB 5; Length 73;  
 Best Local Similarity 87.5%; Pred. No. 9.4e-27;  
 Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 APANPCCDAATCKLKLRTGSQCAGLCCQCKMKEGIVCRARRGGDDDDYCNIGISAGCPRN 61  
 Db 10 SPGNPCCDAATCKLROGAQCAEGLCCQCRMKEGTCRMRGDDDDYCNIGISAGCPRN 69  
 QY 62 PFHA 65  
 Db 70 PFHA 73  
 RESULT 6  
 AAE19787  
 ID AAE19787 standard; protein; 73 AA.  
 AC AAE19787;  
 XX DT 29-AUG-2003 (revised)  
 DT 07-AUG-2003 (revised)  
 DT 18-JUN-2002 (first entry)  
 DE Agkistrodon saxatilis emelianov saxatilin protein.  
 XX KW Korean snake; saxatilin; anticoagulant; cytostatic; venom; anti-tumour;  
 KW platelet aggregation; angiogenesis; cytotoxicity.  
 XX OS Gloydius halys.  
 XX FH Key Locality/Qualifiers  
 FT Misc-difference 1. 3  
 FT /note= "Encoded by GGA"  
 XX WO200214488-A1.  
 XX PD 21-FEB-2002.  
 XX PR 26-JUL-2000; 2000WO-KR000809.  
 XX PR 26-JUL-2000; 2000WO-KR000809.  
 XX (CHUN/) CHUNG K.  
 PA (KIMD/) KIM D.  
 XX PI Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;  
 XX DR WPI; 2002-241903/29.  
 DR N-PSDB; AAD31060.  
 XX PT New cDNA encoding Saxatilin Protein derived from venom of Korean snake  
 PT Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation  
 PT agent and anti-tumour agent.  
 XX PS Claim 2; Page 35; 41pp; English.  
 XX CC The invention relates to a cDNA encoding Saxatilin protein derived from  
 CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful  
 CC for as an anti-tumour agent and for effectively suppressing platelet

CC aggregation which makes it possible as and an active ingredient of anti-  
 CC platelet agent. Saxatilin is useful for inhibiting angiogenesis induced  
 CC by tumour and for inhibiting tumour without cytotoxicity. The present  
 CC sequence is Agkistrodon saxatilis emelianov saxatilin protein. (Updated  
 CC on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 73 AA;  
 Query Match 90.3%; Score 345; DB 5; Length 73;  
 Best Local Similarity 87.5%; Pred. No. 1.2e-26;  
 Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 APANPCCDAATCKLKLRTGSQCAGLCCQCKMKEGIVCRARRGGDDDDYCNIGISAGCPRN 61  
 Db 10 SPGNPCCDAATCKLROGAQCAEGLCCQCRMKEGTCRMRGDDDDYCNIGISAGCPRN 69  
 QY 62 PFHA 65  
 Db 70 PFHA 73  
 RESULT 7  
 AAR06494  
 ID AAR06494 standard; protein; 73 AA.  
 AC AAR06494;  
 XX DT 25-MAR-2003 (revised)  
 DT 04-JAN-1991 (first entry)  
 DE Platelet aggregation inhibitor.  
 XX KW Snake venom; thromboxan A2; thrombosis; anti-coagulant.  
 XX OS Synthetic.  
 XX PN WO9008772-A.  
 XX PD 09-AUG-1990.  
 XX PP 27-JAN-1989; 89US-00303585.  
 XX PR 27-JAN-1989; 89US-00303590.  
 PR 01-NOV-1989; 89US-00430313.  
 XX PA (UYBO-) UNIV BOSTON  
 PA (BIOJ) BIOPEN INC.  
 PT Maraganore J, Jakubowski J, Chao B;  
 XX DR WPI; 1990-260891/34.  
 DR N-PSDB; AADQ05730.  
 XX PT Pure platelet activation inhibiting polypeptide from snake venom - used  
 PT for preventing agglutination and release in vivo or vitro, and new  
 PT recombinant dna encoding it.  
 XX PS Claim 3; Fig 9; 73pp; English.  
 XX The sequence is deduced from the coding strand of a synthetic gene for a  
 CC polypeptide inhibitor of platelet activation. The polypeptide is  
 CC analogous to that obt'd. from the venom of Agkistrodon p. piscivorus  
 CC (North American Water Moccasin). The gene can be used to produce  
 recombinant inhibitor or fusion protein with e.g. hirudin derivs. These  
 CC can be used to decrease/ inhibit platelet aggregation and release in vivo  
 CC or in vitro. Usual dose is 0.01-1.0 mg/kg body wt. The recombinant  
 CC protein can also be used to coat the surfaces of invasive medical  
 CC devices. It can also block stenosis and spasm at the site of thrombosis  
 CC by inhibiting the release of thromboxan A2.). See also ARO6508. (Updated  
 CC on 25-MAR-2003 to correct PA field.)

SQ	Sequence 73 AA;	QY	62 PFHA 65
Query Match	88.2%; Score 337; DB 2; Length 73;	Db	70 PLHA 73
Best Local Similarity	87.3%; Pred. No. 7. 2e-26;	Matches	55; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY	2 APANPCDAACKLKGQSQAGLGLCQCKFKEGTIVRRARGDDDDYNGISAGCPRN 61	QY	2 APANPCDAACKLKGQSQAGLGLCQCKFKEGTIVRRARGDDDDYNGISAGCPRN 61
Db	11 SPANPCDAACKLKGQSQAGLGLCQCKFKEGTIVRRARGDDDDYNGISAGCPRN 70	Db	10 SPANPCDAACKLKGQSQAGLGLCQCKFKEGTIVRRARGDDDDYNGISAGCPRN 69
QY	62 PFH 64	QY	62 PFH 64
Db	71 PFH 73	Db	70 PLHA 73
RESULT 8		RESULT 9	
AAR06395	standard; protein; 73 AA.	AAR10106	standard; protein; 73 AA.
ID	AAR06395	ID	AAR10106
XX		XX	
AC	AAR06395;	AC	AAR10106
XX		XX	
DT	25-MAR-2003 (revised)	DT	25-MAR-2003 (revised)
13-DEC-1990	(first entry)	13-DEC-1990	(first entry)
XX		XX	
DB	Albolabrin.	DB	Albolabrin.
XX		XX	
KW	Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;	KW	Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;
KW	Viper venom.	KW	Viper venom.
OS	Trimeresurus albolabris.	OS	Trimeresurus albolabris.
XX		XX	
PN	BP382451-A.	PN	BP382451-A.
XX		XX	
PD	16-AUG-1990.	PD	16-AUG-1990.
XX		XX	
PF	05-FEB-1990; 90EP-00301181.	PF	05-FEB-1990; 90EP-00301181.
XX		XX	
PR	07-FEB-1999; 89US-00307642.	PR	07-FEB-1999; 89US-00307642.
XX		XX	
PA	(MERCK ) MERCK & CO INC.	PA	(MERCK ) MERCK & CO INC.
PA	(UTEM ) UNIV TEMPLE	PA	(UTEM ) UNIV TEMPLE
PA	(FRIE ) FRIEDMAN P A.	PA	(FRIE ) FRIEDMAN P A.
XX		XX	
PI	Friedman PA, Jacobs JW, Gould RJ, Polokoff MA, Gan ZR;	PI	Friedman PA, Jacobs JW, Gould RJ, Polokoff MA, Gan ZR;
PI	Niewiarowa S, Holt JC, Rucinski B;	PI	Niewiarowa S, Holt JC, Rucinski B;
XX		XX	
DR	WPI; 1990-248351/33.	DR	WPI; 1990-248351/33.
XX		XX	
PT	Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding to human platelets and inhibiting fibrinogen-induced aggregation.	PT	Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding to human platelets and inhibiting fibrinogen-induced aggregation.
PT		PT	
XX		XX	
PS	Claim 2; Page 13; 1pp; English.	PS	Claim 2; Page 13; 1pp; English.
XX		XX	
CC	The peptide is prep'd. from the venom of the viper <i>T. albolabris</i> or may be prep'd. by genetic engineering or solid phase synthesis. It inhibits both fibrin binding to human platelets and fibrinogen-induced aggregation of human platelets. It is eliminated from the circulation rapidly and is therefore useful in situations where a strong antithrombotic action of short duration is needed, e.g. in surgery on peripheral arteries, in cardiovascular surgery and the interaction of platelets with artificial surfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct PA field.)	CC	The peptide is prep'd. from the venom of the viper <i>T. albolabris</i> or may be prep'd. by genetic engineering or solid phase synthesis. It inhibits both fibrin binding to human platelets and fibrinogen-induced aggregation of human platelets. It is eliminated from the circulation rapidly and is therefore useful in situations where a strong antithrombotic action of short duration is needed, e.g. in surgery on peripheral arteries, in cardiovascular surgery and the interaction of platelets with artificial surfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct PA field.)
SQ	Sequence 73 AA;	SQ	Sequence 73 AA;
RESULT 10		RESULT 10	
AAR53946		AAR53946	
ID	AAR53946 standard; peptide; 73 AA.	ID	AAR53946 standard; peptide; 73 AA.
XX		XX	
AC	AAR53946;	AC	AAR53946;
XX		XX	
DT	27-Aug-2003 (revised)	DT	27-Aug-2003 (revised)
25-MAR-2003 (revised)		25-MAR-2003 (revised)	
21-DEC-1994	(first entry)	21-DEC-1994	(first entry)
XX		XX	
DE	Disintegrin peptide #14.	DE	Disintegrin peptide #14.
XX		XX	
KW	Disintegrin; viperidae; snake; integrin; inhibitor; fibrinogen;	KW	Disintegrin; viperidae; snake; integrin; inhibitor; fibrinogen;



PD 01-OCT-1998.  
 XX  
 PF 25-FEB-1998; 98WO-US003632.  
 XX  
 PR 21-MAR-1997; 97US-00823791.  
 XX  
 PR 06-MAY-1997; 97US-00851780.  
 PR 18-JUN-1997; 97US-00877826.  
 PR 02-JUL-1997; 97US-00887215.  
 PR 08-SEP-1997; 97US-00925353.  
 XX  
 PA (IMAR-) IMARK PHARM CORP.  
 XX  
 PI Unger BC;  
 XX  
 PT Processes for drug delivery, therapeutic imaging and diagnostic imaging -  
 PT comprises use of compositions comprising charged lipid, counter-ion and  
 PT lipid covalently bonded to polymer.  
 PS Disclosure; Page 68; 167pp; English.  
 XX  
 CC The invention relates to a method of: (A) delivering a bioactive agent  
 CC (BA) to a patient by: (a) administering a composition comprising: (i) an  
 CC anionic lipid (AL); (ii) a cationic counter ion (CCI); (iii) a lipid  
 CC covalently bonded to a polymer (LBP), and (iv) BA, and (b) applying  
 CC therapeutic ultrasound to facilitate delivery of BA in a desired region;  
 CC (B) delivering a BA to a patient, comprising administering a composition  
 CC comprising a charged lipid (CL), a counter ion (CT), LBP, BA and  
 CC targeting ligand (TL); (C) providing an image of an internal region of a  
 CC patient, comprising: (a) administering a composition comprising CL, CT  
 CC and LBP of the composition in (B), and (b) scanning the patient using  
 CC diagnostic imaging, to give visible images of the region, and  
 CC contrast agent comprising components in (C). The  
 CC targeted drug delivery, therapeutic imaging and diagnostic imaging, this  
 CC sequence represents an example of a targeting ligand designated  
 XX  
 SQ Sequence 73 AA;

Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLUTTESQAGLCCPCKFMKEGTVCRRARGDDDDYCNGISAGCPRN 61  
 Db 10 SPANPCDAATCKLUTTESQAGLCCPCKFMKEGTVCRRARGDDDDYCNGISAGCPRN 69

RESULT 13  
 AAB20598  
 ID AAB20598 standard; peptide: 73 AA.  
 XX  
 AC AAB20598;  
 XX  
 DT 12-DEC-2000 (first entry)  
 XX  
 DE Albolabrin targeting ligand peptide.

Targeting ligand peptide; imaging; ultrasound; vesicle; tumour;  
 KW myocardial; endothelial; epithelial; glycoprotein GplbIIIA receptor;  
 KW detection; thrombus; integrin; malignancy; inflammation; lesion;  
 KW atherosclerotic plaque; carcinoma.  
 OS Unidentified.

XX  
 PN WO20045856-A2.

PD 10-AUG-2000.  
 XX  
 PF 02-FEB-2000; 2000WO-US002620.  
 XX  
 PR 03-FEB-1999; 99US-00243640.  
 XX  
 PA (IMAR-) IMARK PHARM CORP.  
 PI Unger BC, Wu Y;  
 XX  
 DR WPI; 2000-532867/48.  
 XX  
 PT Ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas,  
 PT uses different types of energy for priming and interrogating the subject.  
 XX  
 PS Disclosure; Page 70; 21pp; English.  
 XX  
 CC The Present invention describes an ultrasound method comprising: (i)  
 CC administering a targeted vesicle composition (A); and (ii) scanning the  
 CC subject by exposure to a first type of ultrasound energy, and then  
 CC interrogating with a second type of ultrasound energy. (A) consists of a  
 CC vesicle comprising a lipid, protein or polymer, encapsulating a gas, in  
 CC combination with a targeting ligand. The method is used to detect: (I) a  
 CC thrombus (particularly old or echogenic); (II) a low concentration of  
 CC vesicles; or (III) vesicles targeted to endothelial tissue, particularly  
 CC those containing integrins associated with malignancy or inflammation in  
 CC early or small lesions, e.g. atherosclerotic plaque or ovarian  
 CC endometrial or other carcinomas. The method increases the signal from  
 CC microbubbles and reduces background noise. The present sequence  
 CC represents a targeting ligand peptide which is used in the method of the  
 CC present invention  
 XX  
 SQ Sequence 73 AA;

Query Match 87.4%; Score 334; DB 3; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLUTTESQAGLCCPCKFMKEGTVCRRARGDDDDYCNGISAGCPRN 61  
 Db 10 SPANPCDAATCKLUTTESQAGLCCPCKFMKEGTVCRRARGDDDDYCNGISAGCPRN 69

RESULT 14  
 ABG30392  
 ID ABG30392 standard; protein; 73 AA.  
 XX  
 AC ABG30392;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Glycoprotein GplbIIIA targeting ligand Albolabrin.  
 XX  
 KW Target vesicle; diagnostic imaging; thrombus; cancer; albolabrin;  
 KW arteriosclerosis; atherosclerotic plaque; infarcted myocardium;  
 KW glycoprotein GplbIIIA receptor; targeting ligand.  
 XX  
 OS Unidentified.  
 XX  
 PN WO20036161-A2.  
 PD 10-MAY-2002.  
 XX  
 PF 17-OCT-2001; 2001WO-US032308.  
 XX  
 PR 30-OCT-2000; 2000US-00693679.  
 XX  
 PA (IMAR-) IMARK THERAPEUTICS INC.

PI Unger EC, Matsunaga TO, Schumann PA;

XX DR WPI; 2002-489986/52.

XX PT New targeted compound useful in target vesicle composition for imaging a thrombus in a region of a patient having a combination of hydrophobic compound, hydrophilic polymer and targeting ligand.

XX PS Disclosure; Page 68; 206pp; English.

CC CC This invention relates to a novel targeted compound having a combination of hydrophobic compound, hydrophilic polymer and targeting ligand. The invention also comprises a target vesicle composition comprising lipid, protein or polymer gas filled vesicles in an aqueous carrier, a method for imaging a thrombus in a region of a patient involving administering to the patient a target vehicle composition and scanning the region (preferably cardiac region) with diagnostic imaging (preferably diagnostic ultrasound) and a method for lysing a thrombus in a blood vessel. The invention also comprises a method for providing an image of an internal region of a patient which can be used to obtain a visible image of a region (preferably arteriosclerosis, atherosclerotic plaque, infarcted myocardium or a cancer cell) and a method for diagnosing the presence of disease tissue in a patient involving administering a target vehicle composition and scanning the patient using ultrasound to obtain a visible image of the region. The methods of the invention may be used for imaging a thrombus in a region of a patient, lysing a thrombus in a blood vessel, diagnosing the presence of diseased tissue in a patient and for the therapeutic delivery in vivo of a bioactive agent. The compounds of the invention are easily synthesised and have diagnostic efficacy, enhanced biocompatibility and/or improved targeting efficacy over prior art methods. The present sequence represents a glycoprotein GPRINIA receptor targeting ligand albolabrin used in the method of the invention

CC CC Sequence 73 AA;

CC CC

Query Match 87.4%; Score 334; DB 5; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25; Mismatches 5; Indels 0; Gaps 0;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLUTGSQAGDGLCQCKEMKEGTIVCRRARGDDIDYNGISAGCPRN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 10 SPANPCDAATCKLUPGQQGEGLCCQCSMFKGTCRRARGDDIDYNGISAGCPRN 69

Qy 62 PPFA 65  
 Db 70 PLHA 73

Sequence 73 AA;

RESULT 15  
 ABU63163 ID ABU63163 standard; protein; 73 AA.  
 XX AC ABU63163;  
 XX DT 17-SEP-2003 (first entry)  
 XX DE Targeting ligand #13 used in novel diagnostic ultrabound method.

Qy 2 APANPCDAATCKLUTGSQAGDGLCQCKEMKEGTIVCRRARGDDIDYNGISAGCPRN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 10 SPANPCDAATCKLUPGQQGEGLCCQCSMFKGTCRRARGDDIDYNGISAGCPRN 69

Qy 62 PPFA 65  
 Db 70 PLHA 73

Search completed: November 3, 2005, 08:15:50  
 Job time : 75 sec<sup>b</sup>

OS Synthetic.  
 XX PN US6521211-B1.  
 XX PD 18-FEB-2003.  
 XX PP 03-FEB-1999; 99US-00243640.

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:12:57 ; Search time 39 Seconds  
(without alignments)

160.361 Million cell updates/sec

title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382

Sequence: 1 DAPANPCDAATCKLTTGSQ. .... DUDDYCNGISAGCPRNPFHA 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.0

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length	DB	ID	Description
1	346	90.6	71	2	AS9409	platelet-aggregation disintegrin (brevicaudin) 2b, venom - <i>Gloydius halys brevicaudus</i>
2	336	88.0	484	2	JCB8020	metalloprotease - metalloprotease
3	334	87.4	73	2	A23731	albolaibrin - green
4	334	87.4	73	2	E35982	trigamin gamma -
5	333	87.2	71	2	A59411	platelet-aggregati
6	333	87.2	73	2	A59410	platelet aggregati
7	326	85.3	73	2	D35982	trigamin beta-2 -
8	322	84.3	480	1	A33065	trigamin - precursor
9	321.5	84.2	71	2	A23990	appilaggin - easter
10	286	74.9	71	2	A33019	platelet aggregati
11	286	74.9	72	2	A33019	platelet aggregati
12	285	74.6	73	2	H33019	platelet aggregati
13	282	73.8	72	2	B43020	platelet aggregati
14	276	73.3	73	2	A23019	platelet aggregati
15	272	71.2	73	2	B40003	platelet aggregati
16	270	70.7	73	2	A33020	platelet aggregati
17	269	70.4	72	2	A33019	platelet aggregati
18	269	70.4	72	2	B43019	platelet aggregati
19	269	70.4	72	2	D43019	platelet aggregati
20	268	70.2	73	2	C3019	platelet aggregati
21	266	69.6	73	2	A4301	platelet aggregati
22	264	69.1	73	2	A40003	platelet aggregati
23	263	68.8	71	2	A59412	K2P-bearing platelet
24	261	68.3	481	2	S43125	trumucin precursor
25	260	68.1	71	2	A29413	platelet-aggregati
26	257	67.3	71	2	S13168	batroxostatin - ba
27	251	65.9	481	2	JG4342	fibinolytic pro
28	244	64.9	70	2	A88649	flavofuridin Ivalida
29	241	63.1	75	2	JX0169	cytotoxic factor I

RESULT 1

AS9409

platelet-aggregation disintegrin (brevicaudin) 2b, venom - *Gloydius halys brevicaudus*

C-Species: *Gloydius halys brevicaudus*

C-Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004

C-Accesion: A59409

R-Terada, S.

Fukuoka Univ. Sci. Reports 30, 71-78, 2000

A-Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from *Gloydius halys brevicaudus*

A-Reference number: A59409

A-Accesion: A59409

A-Status: preliminary

A-Molecule type: protein

A-Residues: 1-71 <TER>

A-Cross-references: UNIPROT:090wco

C-Keywords: anticoagulant, integrin inhibitor, venom

Query Match 90.6%; Score 346; DB 2; Length 71;

Best local Similarity 87.5%; Pred. No. 3.2e-27; Mismatches 3; Indels 0; Gaps 0;

Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy	Db	Qy	Db
2 APANPCDAATCKLTTGSQACAGIICDQCKFMKGTVCRARGDDDDYNGISAGCPRN	61	8 SPGNPPCCDATCKLURQGAQCAEGIICDQCRPMKEGTICRRARGDDDDYNGISAGCPRN	67
:    <p>RESULT 2</p> <p>JCB8020</p> <p>metalloprotease-disintegrin protein, Jerdonitin - <i>Trimeresurus jerdoni</i></p> <p>C-Species: <i>Trimeresurus jerdoni</i></p> <p>C-Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004</p> <p>C-Accesion: JCB8020; PCT7231</p> <p>R-Chen, R.-Q.; Jin, Y.; Wu, J.-B.; Zhou, X.-D.; Lu, Q.-M.; Wang, W.-Y.; Xiong, Y.-L.</p> <p>Biochem. Biophys. Res. Commun. 310, 182-187, 2003</p> <p>A-Title: A new protein structure of P-II class snake venom metalloproteinases: It contains a proline-rich domain</p> <p>A-Reference number: JCB8020; PMID: 14511668</p> <p>A-Accesion: JCB8020</p> <p>A-Molecule type: mRNA</p> <p>A-Residues: 1-484 &lt;CHE&gt;</p> <p>A-Cross-references: GB:AY3564231</p> <p>A-Experimental source: Crude venom</p> <p>A-Accession: PCT7231</p> <p>A-Molecule type: protein</p> <p>A-Residues: 206-214,221-233,299-308,310-344,451-453,460-484 &lt;CH2&gt;</p> <p>C-Comment: This protein, a new metalloproteinase-disintegrin protein, belongs to the ICB50 of 120mM. It contains a proline-rich domain</p> <p>C-Keywords: Jerdonitin; metalloproteinase-disintegrin; platelet aggregation; SVMP</p>			

Query Match 89.0%; Score 336; DB 2; Length 484;  
 Best Local Similarity 90.2%; Pred. No. 1.2e-25;  
 Matches 55; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 NPCCDAATCKLTGSGQCADGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRNPH 64  
 Db 424 NPCCDAATCKLTGSGQCADGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRNPH 483  
 Qy 65 A 65  
 Db 484 A 484

## RESULT 3

A23731  
 albolabrin - green pit viper  
 C;Species: *Trimeresurus albolabris* (green pit viper)  
 C;Date: 28-Feb-1992 #sequence\_revision 22-Aug-1997 #text\_change 09-Jul-2004  
 C;Accession: A23731; S43021  
 R;Calvete, J.J.; Scheifele, W.; Sobzka, T.; Lu, W.; Cook, J.J.; Jameson, B.A.; Niewiarows  
 Biochemistry 30, 5225-5229, 1991  
 A;Title: Identification of the disulfide bond pattern in albolabrin, an RGD-containing pro  
 tein activity  
 A;Reference number: A23731; MUID:91242430; PMID:2036389  
 A;Accession: A23731  
 A;Molecule type: protein  
 A;Residues: 1-73 <CAL>  
 A;Cross-references: UNIPROT:PI1496  
 R;Jasuja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.I.  
 Eur. J. Biochem. 218, 853-860, 1993  
 A;Title: <sup>1</sup>H-NMR studies and secondary structure of the RGD-containing snake toxin, albo  
 A;Reference number: S43021; MUID:9109384; PMID:8281937  
 A;Accession: A59409  
 A;Status: preliminary  
 A;Residues: 1-73 <JAS>  
 C;Function:  
 A;Description: inhibits cell adhesion and platelet aggregation  
 C;Superfamily: unassigned disintegrins; disintegrin homology  
 C;Keywords: venom

F;1-69/Domain: disintegrin homology (fragment) <DIS>  
 F;51-53/Region: cell attachment (R-G-D) motif

Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 4.8e-26;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTGSGQCADGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRN 61  
 Db 10 SPANPCDAATCKLTGSGQCADGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRN 69

Qy 62 PRHA 65  
 Db 70 PRHA 73

## RESULT 5

A59411  
 platelet-aggregation disintegrin (brevicaudin) 1a - *Gloydius halys* brevicaudus  
 C;Species: *Gloydius halys* brevicaudus  
 C;Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004  
 C;Accession: A59411  
 R;Terada, S.  
 Fukuoka Univ. Sci. Reports 30, 71-78, 2000  
 A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from *Gloydi*  
 A;Reference number: A59409  
 A;Accession: A59411  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-71 <TR>  
 A;Cross-references: UNIPROT:Q90220  
 C;Keywords: anticoagulant; integrin inhibitor; venom

Query Match 87.2%; Score 333; DB 2; Length 71;  
 Best Local Similarity 84.4%; Pred. No. 5.9e-26;  
 Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTGSGQCADGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRN 61  
 Db 8 SPGNPCDAATCKLROGAQCAEGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRN 67

Qy 62 PRHA 65  
 Db 68 PRHA 71

## RESULT 6

A59410  
 platelet aggregation disintegrin (brevicaudin) 1b, venom - *Gloydius halys* brevicaudus  
 C;Species: *Gloydius halys* brevicaudus  
 C;Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004  
 C;Accession: A59410  
 R;Terada, S.  
 Fukuoka Univ. Sci. Reports 30, 71-78, 2000  
 A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from *Gloydi*  
 A;Reference number: A59409  
 A;Accession: A59410  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-73 <TR>  
 A;Cross-references: UNIPROT:Q90220  
 C;Keywords: anticoagulant; integrin inhibitor; venom

Query Match 87.2%; Score 333; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 6e-26;  
 Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTGSGQCADGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRN 61  
 Db 10 SPGNPCDAATCKLROGAQCAEGLCCDQCKFMKEGTVCRRARGDDDDYCNISAGCPRN 69

Qy 62 PRHA 65

## RESULT 4

E35982  
 trigamin gamma - Indian green tree viper  
 C;Species: *Trimeresurus gramineus* (Indian green tree viper)  
 C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Aug-2004  
 C;Accession: E35982  
 R;Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; Bu  
 Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990  
 A;Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence  
 A;Reference number: A35982; MUID:90207217; PMID:2320569  
 A;Accession: E35982  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-73 <DEN>  
 A;Cross-references: UNIPROT:PI1496  
 C;Superfamily: disintegrin homology

Db	70 PFHA 73	F;1-18/Domain: signal sequence #status predicted <SIG> F;398-476/Domain: disintegrin homology <DIS> F;408-479/Domain: disintegrin homology experimental <MAT> F;45-460/Region: cell attachment (R-G-D) motif F;279/Binding site: carbohydrate (Asn) (covalent) #status predicted F;333-337/343/Binding site: zinc (H2b) #status predicted
RESULT 7		N/Contains: trigramin beta-2 - Indian green tree viper C.Species: <i>Trimeresurus gramineus</i> (Indian green tree viper) C.Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004 C.Accession: D35982; C15982 R.Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; Bu Proc. Natl. Acad. Sci. U.S.A. 87: 2471-2475, 1990 A.Title: Platelet glycoprotein Ib-IIIa protein antagonists from snake venoms: evidence A.Reference number: A35982; MUID:90207217; PMID:2320569 A.Molecule type: protein A.Residues: 1-73 <DEN> A.Cross-references: UNIPROT:PI17495 A.Accession: C35982 A.Molecule type: protein A.Residues: 1-72 <DE2> C:Superfamily: disintegrin homology C.Keywords: venom F1-72/Product: trigramin beta-2 #status experimental <MA2> F1-72/Domain: disintegrin homology (fragment) <DIS> F1-53/Region: cell attachment (R-G-D) motif
Query Match	85.3%; Score 326; DB 2; Length 73; Best Local Similarity 82.8%; Pred. No. 2.8e-24; Matches 53; Conservative 5; Indels 0; Gaps 0;	Query Match 84.3%; Score 322; DB 1; Length 480; Best Local Similarity 82.8%; Pred. No. 2.8e-24; Matches 53; Conservative 5; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLUTTGQQCADGLCCKFMKGTVRRARGDDDDYNGISAGCPRN 61 Db 10 SPANPCCDATCKLUPGAGCCEGPGCDQCSFMKKGTCRRARGDDDDYNGRSAGCPRN 69	Qy 2 APANPCCDATCKLUTTGQQCADGLCCKFMKGTVRRARGDDDDYNGISAGCPRN 61 Db 10 SPANPCCDATCKLUPGAGCCEGPGCDQCSFMKKGTCRRARGDDDDYNGRSAGCPRN 476
Qy	62 PFHA 65	Qy 62 PFHA 65
Db	70 PFHA 73	Db 477 PFHA 480

RESULT 8		RESULT 9
A30065		A33990
N/Contains: hemorrhagic proteinase (EC 3.4.24.-); platelet aggregation inhibitor (disint		C.Species: <i>Agkistrodon piscivorus piscivorus</i> (eastern cottonmouth)
C.Species: <i>Trimeresurus gramineus</i> (Indian green tree viper)		C.Accession: A33990
C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004		R;Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chow, E.P.; Marzec, U.M.; Harker, L.A.; Mar.
C.Accession: S12589; A30065; A22784		Proc. Natl. Acad. Sci. U.S.A. 86: 8050-8054, 1989
R.Nepper, M.P.; Jacobson, M.A.		A.Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a potent inhi
Nucleic Acids Res. 18, 4255, 1990		A.Reference number: A33990; MUID:90046735; PMID:2510158
A.Reference: Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin.		A.Status: preliminary
A.Accession: S12589		A.Molecule type: protein
A.Molecule type: mRNA		A.Residues: 1-71 <CHA>
A.Residues: 1-480 <NEB>		A.Cross-references: UNIPROT:PI16338
A.Cross-references: UNIPROT:P15503; EMBL:X51530; MIP:964407; PID:964408		C:Superfamily: unassigned disintegrins; disintegrin homology
A.Note: translation of the signal sequence and the mature protein but not of the propept		F;1-68/Domain: disintegrin homology (fragment) <DIS>
R.Huang, T.F.; Holt, J.C.; Kirby, E.P.; Niewiarowski, S.		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
Biocchemistry 28, 661-666, 1989		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Title: Trigramin: primary structure and its inhibition of von Willebrand factor bindir		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Reference number: A30065; MUID:89229063; PMID:2653425		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Accession: A30065		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Molecule type: protein		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Residues: 408-479 <HUA>		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
R.Huang, T.F.; Holt, J.C.; Lukasiewicz, H.; Niewiarowski, S.		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
J. Biol. Chem. 262, 16157-16163, 1987		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Title: Trigramin. A low molecular weight peptide inhibiting fibrinogen interaction wit		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Reference number: A29784; MUID:89058981; PMID:3680247		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Molecule type: protein		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
A.Residues: 408-419 <HUA>		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
C:Superfamily: trigramin precursor; disintegrin homology		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;
C.Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc; zymo		Query Match 84.2%; Score 321.5; DB 2; Length 71; Best Local Similarity 85.7%; Pred. No. 7.8e-25; Matches 54; Conservative 5; Indels 1; Gaps 1;

Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Crotalus basiliscus basiliscus (Mexican West-Coast rattlesnake)
C.Date	12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C.Accession	I43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993	A.Title: Characterization of the integrin specificities of disintegrins isolated from Am. Rattlesnake. A:Reference number: A43019; MUID: 93123215; PMID: 8419314
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31981
C;Superfamily	disintegrin homology <DIS>
F;2-68/Domain	disintegrin homology
RESULT 11	
Query Match	74.9%; Score 286; DB 2; Length 72;
Best Local Similarity	73.4%; Pred. No. 2.3e-21;
Matches	47; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Crotalus molossus molossus (Northern blacktail rattlesnake)
C.Date	12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C.Accession	I43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993	A.Title: Characterization of the integrin specificities of disintegrins isolated from Am. Rattlesnake. A:Reference number: A43019; MUID: 93123215; PMID: 8419314
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31981
C;Superfamily	disintegrin homology <DIS>
F;2-68/Domain	disintegrin homology
RESULT 12	
Query Match	74.9%; Score 286; DB 2; Length 72;
Best Local Similarity	73.4%; Pred. No. 2.3e-21;
Matches	47; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Crotalus molossus molossus (Northern blacktail rattlesnake)
C.Date	12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C.Accession	I43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993	A.Title: Characterization of the integrin specificities of disintegrins isolated from Am. Rattlesnake. A:Reference number: A43019; MUID: 93123215; PMID: 8419314
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31984
C;Superfamily	disintegrin homology <DIS>
F;3-69/Domain	disintegrin homology
Query Match	74.6%; Score 285; DB 2; Length 73;
Best Local Similarity	73.4%; Pred. No. 2.3e-21;
Matches	47; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Crotalus viridis cerberus (Arizona black rattlesnake)
C.Date	12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C.Accession	I43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993	A.Title: Characterization of the integrin specificities of disintegrins isolated from Am. Rattlesnake. A:Reference number: A43019; MUID: 93123215; PMID: 8419314
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31985
C;Superfamily	unassigned disintegrins; disintegrin homology
F;3-69/Domain	disintegrin homology <DIS>
RESULT 13	
Query Match	73.8%; Score 282; DB 2; Length 72;
Best Local Similarity	73.0%; Pred. No. 5.7e-21;
Matches	46; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Crotalus cerberus (Arizona black rattlesnake)
C.Date	12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C.Accession	I43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993	A.Title: Characterization of the integrin specificities of disintegrins isolated from Am. Rattlesnake. A:Reference number: A43019; MUID: 93123215; PMID: 8419314
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31985
C;Superfamily	unassigned disintegrins; disintegrin homology
F;3-69/Domain	disintegrin homology <DIS>
RESULT 14	
Query Match	73.8%; Score 282; DB 2; Length 72;
Best Local Similarity	73.0%; Pred. No. 5.7e-21;
Matches	46; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Crotalus cerberus (Arizona black rattlesnake)
C.Date	12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C.Accession	I43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993	A.Title: Characterization of the integrin specificities of disintegrins isolated from Am. Rattlesnake. A:Reference number: A43019; MUID: 93123215; PMID: 8419314
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31990
C;Superfamily	disintegrin homology
F;3-69/Domain	disintegrin homology <DIS>
RESULT 15	
Query Match	72.3%; Score 276; DB 2; Length 73;
Best Local Similarity	71.4%; Pred. No. 2.2e-20;
Matches	45; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Sistrurus catenatus terminatus (western massasauga)
C.Date	20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C.Accession	B40003
R.Scarborough, R.M.; Rose, J.W.; Heu, M.A.; Phillips, D.R.; Fried, V.A.; Campbell, A.M., J. Biol. Chem. 266, 9359-9362, 1991	A.Title: Barbourin, A GPIb-IIIa-specific integrin antagonist from the venom of Sistrurus catenatus. A:Reference number: A40003; MUID: 91236695; PMID: 2033037
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31990
C;Superfamily	disintegrin homology
F;3-69/Domain	disintegrin homology
Query Match	74.6%; Score 285; DB 2; Length 73;
Best Local Similarity	73.4%; Pred. No. 2.3e-21;
Matches	47; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy	2 APANPCCDATCKLTGSGQCADGLCDOCCKPMKEGTVCRRARGDDDDYNGISAGCPRN 61
C.Species	Sistrurus catenatus terminatus (western massasauga)
C.Date	20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C.Accession	B40003
R.Scarborough, R.M.; Rose, J.W.; Heu, M.A.; Phillips, D.R.; Fried, V.A.; Campbell, A.M., J. Biol. Chem. 266, 9359-9362, 1991	A.Title: Barbourin, A GPIb-IIIa-specific integrin antagonist from the venom of Sistrurus catenatus. A:Reference number: A40003; MUID: 91236695; PMID: 2033037
A.Status	preliminary
A.Residues	1-72 <SCA>
A.Cross-references	UNIPROT:P31990
C;Superfamily	disintegrin homology
F;3-69/Domain	disintegrin homology

A: Molecule type: protein  
A: Residues: 1-73 <SCA>  
A: Cross-references: UNIPROT:P22828  
C: Superfamily: unassigned disintegrins; disintegrin homology  
F: 3-69/Domain: disintegrin homology <DIS>

Query Match 71.2%; Score 272; DB 2; Length 73;  
Best Local Similarity 78.3%; Pred. No. 5.4e-20;  
Matches 47; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
Qy 2 APANPCCDATCKLUTGSGQADGLCCDQCKFMKEGTIVCRRARGDDLYCNGISAGCPRN 61  
Db 10 SPANPCCDATCKLURPGAQCCADGLCCDQCRFMKGTIVCRVARGDWNDTCTGQSADCPRN 69

Search completed: November 3, 2005, 08:19:35  
Job time : 40 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6			
Run on:	November 3, 2005, 08:10:02 ; Search time 177 Seconds (without alignments)			
Sequence:	188.052 Million cell updates/sec			
Scoring table:	US-10-712-584-2_COPY_419_483			
Gapop:	BLOSUM62 Gapop 10.0 , Gapext 0.5			
Searched:	1612378 seqs, 512079187 residues			
Total number of hits satisfying chosen parameters:	1612378			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries			
Database :	UniProt 03-* 1: uniprot_sprot-* 2: uniprot_trembl:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
result No.	Score	Query Match Length	DB ID	Description
1	382	100.0	483	1 DISB_AGKCO
2	382	100.0	483	1 DISB_AGKCO
3	364	95.3	483	1 DISB_AGKPI
4	364	90.6	105	2 078cp2
5	346	90.6	317	2 090wco
6	345	90.3	73	2 09dgh6
7	345	90.3	117	2 090221
8	345	90.3	482	2 09pvk9
9	342	89.5	505	2 073795
10	340	89.0	477	2 098sp2
11	339	88.7	73	2 07s2d5
12	339	88.7	478	2 07s2d9
13	336	88.0	77	2 080124
14	336	88.0	484	1 DIST_TRIE
15	334	87.4	73	1 DISG_TRIA
16	334	87.4	73	1 DISG_TRIGA
17	333	87.2	89	2 0698k8
18	333	87.2	480	2 090220
19	326	85.3	73	1 DISB_TRIGA
20	324	84.8	481	1 DIS2_TRIEL
21	323	84.6	488	2 08aw7
22	322	84.3	480	1 DISA_TRIGA
23	321.5	84.2	71	1 DISI_AGKPI
24	321	84.0	71	1 DIST_AGKHA
25	291	76.2	71	2 09yh68
26	291	76.2	465	2 09iay7
27	291	76.2	479	2 Q9PWT8
28	291	76.2	479	2 Q9PWT0
29	290	75.9	476	2 Q9YI19
30	287	75.1	73	1 07szd6
31	287	75.1	466	2 Q9i4x6
ALIGNMENTS				
RESULT 1				
DISB_AGKCO	STANDARD;	PRT;	483 AA.	
ID DISB_AGKCO				
AC 0805F6;				
DT 25-OCT-2004 (Rel. 45. Created)				
DT 25-OCT-2004 (Rel. 45. Last sequence update)				
DE Zinc metalloproteinase acostatin beta precursor (EC 3.4.24.-)				
DE [Contains: Disintegrin acostatin beta].				
OS Agkistrodon contortrix contortrix (Southern copperhead).				
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;				
OC Viperidae; Crotalinae; Agkistrodon.				
OX NCBI_TaxID:8713;				
RN [1]				
RP SEQUENCE FROM N.A., SEQUENCE OF 419-482, FUNCTION, COFACTOR, AND				
RP SUBUNIT, TISSUE-VENOM;				
RC PubMed:12450389; DOI:10.1021/bi025876b;				
RA Okuda D., Koike H., Morita T.;				
RT "A new gene structure of the disintegrin family: a subunit of dimeric				
RT disintegrin has a short coding region.";				
RL Biochemistry 41:14248-14254 (2002).				
CC -!- FUNCTION: The metalloprotease is a probable venom zinc protease				
CC that acts in hemorrhage (By similarity).				
CC -!- FUNCTION: Acostatin inhibits fibrinogen interaction with platelet				
CC receptors expressed on glycoprotein Ib-IIIa complex. Acts by				
CC binding to the glycoprotein Ib-IIIa receptor on the platelet				
CC surface and inhibits ADP-induced platelet aggregation in human				
CC platelet rich plasma.				
CC --!- COFACTOR: Binds 1 zinc ion per subunit (By Similarity).				
CC --!- SUBUNIT: Acostatin is a heterodimer of an alpha and a beta				
CC subunit.				
CC --!- SUBCELLULAR LOCATION: Secreted.				
CC --!- TISSUE SPECIFICITY: Expressed by the venom gland.				
CC --!- SIMILARITY: Belongs to the pepidase M12B family.				
CC -!- SIMILARITY: Contains 1 disintegrin domain.				
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CC or send an email to license@isb-sib.ch).				
CC EMBL: AB019940; BAC25945.1; -				
DR HSSP: P15167; IDTH.				
DR Inter-Pro; IPR001762; Disintegrin.				
DR InterPro; IPR00625; Pept_M_Zn_BS.				
DR InterPro; IPR01590; Pepidase_M12B.				
DR InterPro; IPR002870; Peptidase_M12B_N.				
DR Pfam; PF00260; Disintegrin; 1.				
DR Pfam; PF01562; Pep_M12B_prope; 1.				

DR PFam; PF01421; Reprolysin; 1.  
 DR PRINTS; PRO0289; DISINTEGRIN.  
 DR PRODom; PDD00664; Disintegrin; 1.  
 DR SMART; SM0050; DISIN; 1.  
 DR PROSITE; PS50215; ADAM\_MERRO; 1.  
 DR PROSITE; PS50214; DISINTEGRIN2; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 KW Hydrolase; Metal-binding; Mammaloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 20  
 PROPEP 21 191  
 FT CHAIN 192 394  
 ACT SITE 335 338  
 METAL 344 344  
 FT DOMAIN 198 394  
 FT DOMAIN 402 482  
 SITE 461 463  
 METAL 334 334  
 ACT SITE 335 335  
 METAL 338 338  
 FT METAL 419 433  
 DISULFID 309 389  
 DISULFID 349 356  
 DISULFID 425 448  
 DISULFID 426 426  
 DISULFID 431 431  
 DISULFID 439 445  
 DISULFID 444 469  
 DISULFID 457 476  
 SEQUENCE 483 AA; 54025 MW; 6D9192657097121 CRC64;

Query Match 100.0%; Score 382; DB 1; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-33; Mismatches 0; Indels 0; Gaps 0;  
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAPANPCCDAATCKLKLTSQCADGLCCDQCKPKMKEGVCRARGDDDDYNGISAGCPR 60  
 Db 419 DAPANPCCDAATCKLKLTSQCADGLCCDQCKPKMKEGVCRARGDDDDYNGISAGCPR 478

Qy 61 NPFHA 65  
 Db 479 NPFHA 483

RESULT 2

DISI\_AGKCO  
 ID DISI\_AGKCO STANDARD; PRT; 483 AA.  
 AC Q9IAB0;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Zinc metalloproteinase contortrostatin precursor (EC 3.4.24.-)  
 DE [Contains: Disintegrin contortrostatin]  
 DE Agkistrodon contortrix contortrix (Southern copperhead).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutetrapoda;  
 OC Lepidota; Squamata; Sceloplossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Agkistrodon.  
 OX NCBI\_Taxid=8713;  
 RN 11  
 RP SEQUENCE FROM N.A., SEQUENCE OF 419-433, FUNCTION, COFACTOR, AND  
 RP SUBUNIT.  
 RC TISSUE=Venom gland;  
 RX MEDLINE=20166949; PubMed=10700384; DOI=10.1006/abbi.1999.1682;  
 RA Zhou Q., Hu P., Ritter M.R., Swenson S.D., Argounova S., Epstein A.L.,  
 RA Markland F.S.;  
 RT "Molecular cloning and functional expression of contortrostatin, a  
 homodimeric disintegrin from southern copperhead snake venom.",  
 RT Arch. Biochem. Biophys. 375:278-288(2000).  
 CC  
 - FUNCTION: The metalloproteinase is a probable venom zinc protease  
 - that acts in hemorrhage (By similarity).

CC -1 FUNCTION: The disintegrin binds and inhibits integrins alpha-1, beta-3, alpha-5/beta-1, alpha-6/beta-3, and alpha-5/beta-5. It blocks cancer cell adhesion to fibronectin and vitronectin and thus prevent invasion of cancer cells.  
 CC -1 PROTEIN: Binds 1 zinc ion per subunit.  
 CC -1 SUBUNIT: Homodimer; disulfiene-linked (disintegrin).  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1 SIMILARITY: Contains 1 disintegrin domain.

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CC DR EMBL; AF212305; AAF65171.1; --.  
 DR HSSP; P18619; IFLV.  
 DR Interrito; IPR010762; Disintegrin.  
 DR Interrito; IPR00625; Pept\_M\_Zn\_BS.  
 DR Interrito; IPR00590; Peptidase\_M12B.  
 DR Interrito; IPR002870; Peptidase\_M12B\_N.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR Pfam; PF01562; Pept\_M12B\_Propep; 1.  
 DR PRINTS; PRO0289; DISINTEGRIN.  
 DR PRODom; PDD00664; Disintegrin; 1.  
 DR SMART; SM0050; DISIN; 1.  
 DR PROSITE; PS50215; ADAM\_MERRO; 1.  
 DR PROSITE; PS00142; DISINTEGRIN2; 1.  
 DR PROSITE; PS50214; ZINC PROTEASE; 1.  
 KW Blood coagulation; Cell adhesion; Direct protein sequencing; Hydrolase; Metal-binding; Mammaloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 20  
 PROPEP 21 190  
 FT CHAIN 191 394  
 FT SITE 461 463  
 FT METAL 334 334  
 FT ACT SITE 395 335  
 FT DOMAIN 198 394  
 FT DOMAIN 402 482  
 FT METAL 334 338  
 FT METAL 344 344  
 FT DISULFID 309 389  
 FT DISULFID 349 356  
 FT DISULFID 425 448  
 FT DISULFID 439 445  
 FT DISULFID 444 469  
 FT DISULFID 457 476  
 SEQUENCE 483 AA; 53948 MW; 2DBB370PC590007 CRC64;

Query Match 100.0%; Score 382; DB 1; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-33; Mismatches 0; Indels 0; Gaps 0;  
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAPANPCCDAATCKLKLTSQCADGLCCDQCKPKMKEGVCRARGDDDDYNGISAGCPR 60  
 Db 419 DAPANPCCDAATCKLKLTSQCADGLCCDQCKPKMKEGVCRARGDDDDYNGISAGCPR 478

Qy 61 NPFHA 65  
 Db 479 NPFHA 483

RESULT 3

DISB\_AGKPI  
 ID DISB\_AGKPI STANDARD; PRT; 483 AA.

AC	Q805F4;	FT	CHAIN	192	394	Zinc metalloproteinase piscivostatin beta.
DT	25-OCT-2004 (Rel. 45, last sequence update)	FT	PROPEP	395	414	Spacer peptide (Potential) disintegrin piscivostatin beta.
DT	25-OCT-2004 (Rel. 45, last annotation update)	FT	CHAIN	415	483	Disintegrin piscivostatin beta.
DE	Zinc metalloproteinase piscivostatin beta precursor (EC 3.4.24.-)	FT	DOMAIN	198	394	Metalloprotease.
DE	(Contains: Disintegrin piscivostatin beta; Agkistrodon piscivorus piscivorus (Eastern cottonmouth); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosaurs; Squamata; Serpentes; Colubroidea; Viperidae; Crotalinae; Agkistrodon; NCBITaxID=8716; [1])	FT	SITE	461	463	Disintegrin-like.
RP	"SEQUENCE FROM N.A., AND SUBUNIT.	FT	METAL	334	334	Cell attachment site (atypical).
RC	TISSUE:Venom;	FT	ACT SITE	335	335	Zinc (catalytic).
RC	PubMed:12450389; DOI=10.1021/bi0258768;	FT	METAL	338	338	Zinc (catalytic).
RA	Okuda D., Koike H., Morita T.	FT	METAL	344	344	Zinc (catalytic).
RT	"A new gene structure of the disintegrin family: a subunit of dimeric disintegrin has a short coding region.";	FT	DISULFID	309	389	By similarity.
RT	Biochemistry 41:14248-14254 (2002).	FT	DISULFID	349	356	By similarity.
RN	[2]	FT	DISULFID	425	448	By similarity.
RP	SEQUENCE OF 415-483, AND CHARACTERIZATION OF PISCIVOSTATIN BETA.	FT	DISULFID	426	426	Interchain (with C-54 in alpha subunit)
RC	TISSUE:Venom;	FT	DISULFID	431	431	(By similarity).
RX	PubMed:11550017;	FT	DISULFID	439	445	Interchain (with C-59 in alpha subunit)
RA	Okuda D., Morita T.;	FT	DISULFID	444	469	(By similarity).
RT	"Purification and characterization of a new RGD/KGG-containing dimeric disintegrin, piscivostatin, from the venom of Agkistrodon piscivorus piscivorus: the unique effect of piscivostatin on platelet aggregation.";	FT	DISULFID	457	476	By similarity.
RT	J. Biochem. 130:407-415 (2001).	FT	SEQUENCE	483	AA: 54072 MW: 518962 F1D9C6E0F00DE3B7 CRC64;	By similarity.
RL		Query	Match	95.3%	Score 364; DB 1; Length 483;	
CC	-!- SUBUNIT: Piscivostatin is a heterodimer of an alpha and a beta subunit.	Matches	61;	Pred. No. 4 7e-31;	Best Local Similarity 93.8%;	
CC	-!- SUBCELLULAR LOCATION: Secreted.	Conservative	2;	Indels 0;	Mismatches 2;	
CC	-!- FUNCTION: The metalloproteinase is a probable venom zinc protease that acts in hemorrhage (By similarity).	Db	419	61 NPFLHA 65	DB 419 DAPANPCCDAATCKLTTGSQCLAGLDDCKENKEGTVCHRAKGDIDDYNGISACPR 478	
CC	-!- FUNCTION: Piscivostatin inhibits fibrinogen interaction with platelet receptors expressed on glycoprotein IIb-IIIa complex.	QY	479	NPFLHA 483	DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
CC	-!- ACTS BY BINDING TO THE GLYCOPROTEIN IIb-IIIa RECEPTOR ON THE PLATELET SURFACE AND INHIBITS BOTH ADP-INDUCED PLATELET AGGREGATION AND PLATELET	Db	419	NPFLHA 483	DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
CC	-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).	RESULT	4		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
CC	-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).	Q8CP2	078CP2	PRELIMINARY;	PRT; 105 AA.	DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- SUBUNIT: Piscivostatin is a heterodimer of an alpha and a beta subunit.	AC	078CP2;			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- SUBCELLULAR LOCATION: Secreted.	DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- FUNCTION: The metalloproteinase is a probable venom zinc protease that acts in hemorrhage (By similarity).	QY	1	DAPANPCCDAATCKLTTGSQCLAGLDDCKENKEGTVCHRAKGDIDDYNGISACPR 60		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- FUNCTION: Piscivostatin inhibits fibrinogen interaction with platelet receptors expressed on glycoprotein IIb-IIIa complex.	Db	419	DAPANPCCDAATCKLTTGSQCLAGLDDCKENKEGTVCHRAKGDIDDYNGISACPR 478		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- ACTS BY BINDING TO THE GLYCOPROTEIN IIb-IIIa RECEPTOR ON THE PLATELET SURFACE AND INHIBITS BOTH ADP-INDUCED PLATELET AGGREGATION AND PLATELET	QY	61	NPFLHA 65		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- SIMILARITY: Belongs to the peptidase M12B family.	Db	479	NPFLHA 483		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- SIMILARITY: Contains 1 disintegrin domain.	Q8CP2	078CP2	PRELIMINARY;	PRT; 105 AA.	DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	AC	078CP2;			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- EMBL: AB079906; BAC55947.1; -.	DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- HSSP: P15167; IDTH.	QY	1	DAPANPCCDAATCKLTTGSQCLAGLDDCKENKEGTVCHRAKGDIDDYNGISACPR 60		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- Interpro: IPR001762; Disintegrin.	Db	419	DAPANPCCDAATCKLTTGSQCLAGLDDCKENKEGTVCHRAKGDIDDYNGISACPR 478		DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- Interpro: IPR005025; Pept_M_Zn_BS.	GN	Agkistrodon halsys brevicaudus (Korean siamosa snake) (Gloydius halys brevicaudus).			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- Interpro: IPR001590; Peptidase_M12B.	OS	Agkistrodon halsys brevicaudus (Korean siamosa snake) (Gloydius halys brevicaudus).			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- Interpro: IPR002870; Peptidase_M12B_N.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- Pfam: PF00200; Disintegrin_1.	OX	NCBI_TaxID=259325; [1]			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50215; ADAM_MEPRO; 1.	RN	SEQUENCE FROM N.A.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_1; FALSE_NEG.	RA	Kang I.C., Chung K.H., Lee S.J., Moon H.M., Kim D.S.; "Purification and molecular cloning of a platelet aggregation inhibitor from the snake (Agkistrodon halsys brevicaudus) venom."; RT			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	RT	RT inhibitor from the snake (Agkistrodon halsys brevicaudus) venom.";			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50042; ZINC_PROTASE; 1.	RL	Thromb. Res. 0: 0-0 (1998).			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PRODOM: PDO00664; Disintegrin; 1.	DR	EMBL: AF054626; AAC08997.1; -.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PRODOM: PDO00500; DISINT; 1.	DR	GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50215; ADAM_MEPRO; 1.	DR	Interpro: IPR001762; Disintegrin.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_1; FALSE_NEG.	DR	Interpro: IPR001762; Peptidase_M12B.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	DR	Interpro: IPR00511; P: trypsin.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50042; ZINC_PROTASE; 1.	DR	Pfam; PF00200; Disintegrin; 1.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_1; 1.	DR	Pfam; PF01421; Reprolysin; 1.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	DR	PRINTS; PRO0289; DISINTEGRIN.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	DR	PRINTS; PRO0680; PTRFOIL.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	DR	PRODOM; PDO00664; Disintegrin; 1.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	DR	SMART; SM00050; DISINTEGRIN_1; 1.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- PROSITE: PS50214; DISINTEGRIN_2; 1.	DR	PROSITE; PS50214; DISINTEGRIN_1; 1.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- KW Hydrolase; Metallo-binding; Metalloproteinase; Signal; Zinc; Zymogen.	DR	PROSITE; PS50214; DISINTEGRIN_2; 1.			DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC	-!- SIGNAL	FT	NON_TIER	1	1	Potential.
PROPER	21	FT	SEQUENCE	105 AA;	11407 MW;	6F10A4496DD35FF2 CRC64;
PROPER	191	FT				

Query Match 90.6%; Score 346; DB 2; Length 105;  
 Best Local Similarity 87.5%; Pred. No. 1; e-29;  
 Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLUTGSQCAGLCCDCKFMKEGTVCRRARGDDYNGISAGCPRN 61  
 Db 42 SPGNPCDAATCKLURGAQCAEGLCCDQCRFMKEGTICRRARGDDYNGISAGCPRN 101  
 Qy 62 PFHA 65  
 Db 102 PFHA 105

RESULT 5

090WCO PRELIMINARY; PRT; 317 AA.

ID 090WCO  
 AC 090WCO;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Metalloproteinase (Fragment).

GN Name=hx1-1;  
 OS Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys brevicaudus).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scincoglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 OX NCBI\_TaxID=259325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom gland;  
 RA Xilian H.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF367868; AAK7517.1; -.  
 DR PIR; A59409; A55409.  
 DR PDB; 1L3X; NMR; A=245-317.  
 DR GO; GO:000222; P:metalloendopeptidase activity; IEA.  
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR PF01421; Reprolysin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.

DR PRODOM; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR SMART; SM00055; DISIN; 1.  
 DR PROSITE; PS00214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 317 AA; 35109 MW; 9851177BCBB2202B CRC64;

Query Match 90.6%; Score 346; DB 2; Length 317;  
 Best Local Similarity 87.5%; Pred. No. 2; e-29;  
 Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLUTGSQCAGLCCDCKFMKEGTVCRRARGDDYNGISAGCPRN 61  
 Db 254 SPGNPCDAATCKLURGAQCAEGLCCDQCRFMKEGTICRRARGDDYNGISAGCPRN 313  
 Qy 62 PFHA 65  
 Db 314 PFHA 317

RESULT 6

09DGH6 PRELIMINARY; PRT; 73 AA.

ID 09DGH6  
 AC 09DGH6;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Saxatilin (Fragment).

OS Pallas).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 OX NCBI\_TaxID=8714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom gland;  
 RA Chung K.-H., Koh Y.-S., Hong S.-Y., Kim D.-S.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY005480; AAG01882.1; -.  
 DR HSSP; P21859; 1J2L.  
 DR InterPro; IPR001762; Disintegrin.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.  
 DR PRODOM; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00427; DISINTEGRIN 1; 1.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 DR FT NON\_TER 1  
 SQ SEQUENCE 73 AA; 7726 MW; 8F0225BBDS502FET7 CRC64;

Query Match 90.3%; Score 345; DB 2; Length 73;  
 Best Local Similarity 87.5%; Pred. No. 1e-29; 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLUTGSQCAGLCCDCKFMKEGTVCRRARGDDYNGISAGCPRN 61  
 Db 10 APANPCDAATCKLURGAQCAEGLCCDQCRFMKEGTICRRARGDDYNGISAGCPRN 69  
 Qy 62 PFHA 65  
 Db 70 PFHA 73

RESULT 7

090221 PRELIMINARY; PRT; 117 AA.

ID 090221  
 AC 090221;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE preproto-halystatin 2 (Fragment).

OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 OX NCBI\_TaxID=8714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashita Z.;  
 RT "Halystatin, a novel disintegrin from agkistrodon halys, is a potent inhibitor of bone resorption and platelet aggregation.";  
 RL Takeda Kenkyusho Ho 53:39-56 (1994).  
 DR EMBL; D2881; BAA06027.1; -.  
 DR HSSP; P21859; 1J2L.  
 DR MEROPS; M12-134; -.  
 DR GO; GO:0004222; P:metalloendopeptidase activity; IEA.  
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR PF01421; Reprolysin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.  
 DR PRODOM; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00215; ADAM MERPO; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 DR FT NON\_TER 1  
 SQ SEQUENCE 117 AA; 12686 MW; B1F9A98056BAB07B CRC64;

Query Match 90.3%; Score 345; DB 2; Length 117;



RN [1] SEQUENCE FROM N.A.  
 RP Best Local Similarity 88.7%; Score 339; DB 2; Length 73;  
 RA Sequence; IEA.  
 RA Silva C.A., Martins de Camargo A.C., de Toledo Serrano S.M.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF345931; RAK15542.1; -.  
 DR GO; GO:001590; C:ribosome; IEA.  
 DR GO; GO:003840; C:ribosome; IEA.  
 DR GO; GO:000422; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:001735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:005412; P:protein biosynthesis; IEA.  
 DR GO; GO:000508; P:proteinolysis and peptidolysis; IEA.  
 DR Interpro; IPR01762; Disintegrin.  
 DR Interpro; IPR01590; Peptidase\_M12B.  
 DR Interpro; IPR003870; Peptidase\_M12B\_N.  
 DR Interpro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Interpro; IPR01515; Ribosomal\_L32E.  
 DR Pfam; PF01421; Reprolysin; 1.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.  
 DR Prodom; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR PROSITE; PS050214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN\_1.  
 SQ SEQUENCE 477 AA; 53440 MW; AC973EE7769E10B3 CRC64;

Query Match 89.0%; Score 340; DB 2; Length 477;  
 Best Local Similarity 87.3%; Pred. No. 1; 8e-28;  
 Matches 55; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PANPCCDAATCKLTGSGCAGDGLCCDOCKFMEGTVCRRGDDYNGISAGCPR 62  
 Db 415 PGNPCCDAATCKLRPGAGCAEGGCCDQDRPMEGTVCRRGDDYNGISAGCPRN 474

Oy 63 PHA 65  
 Db 475 PHA 477

RESULT 11

07S2D5 PRELIMINARY; PRT; 73 AA.

AC 07S2D5; DR Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 26, Last annotation update)  
 DR EMBL; AY004245; AAP20640.1; -.  
 DR HSSP; P21859; IJ2L.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:000735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:000729; P:integrin-mediated signaling pathway; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR GO; GO:000508; P:proteinolysis and peptidolysis; IEA.  
 DR Interpro; IPR01762; Disintegrin.  
 DR Interpro; IPR003870; Peptidase\_M12B.  
 DR Interpro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Interpro; IPR001515; Ribosomal\_L32E.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR Pfam; PF01421; Reprolysin; 1.  
 DR Prodom; PD000664; DISIN; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00215; ADAM\_MERRO; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR PROSITE; PS050214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Integrin.  
 SQ SEQUENCE 478 AA; 53443 MW; CD2FBC975F62A771 CRC64;

Query Match 88.7%; Score 339; DB 2; Length 478;  
 Best Local Similarity 84.6%; Pred. No. 4.5e-29;  
 Matches 55; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Oy 1 DAPANCCDAATCKLTGSGCAGDGLCCDOCKFMEGTVCRRGDDYNGISAGCPR 60  
 Db 414 DSGPNCPCDAATCKLRPGAGCAEGGCCQCRFMKEGTVCRRGDDYNGISAGCPR 473

Oy 61 NPCHA 65  
 Db 474 NPCHA 478

RESULT 13

080124 PRELIMINARY; PRT; 77 AA.

RN SEQUENCE FROM N.A.  
 RA TISSUE-Snake venom gland;  
 RA Sun D.-J., Yang T.-S.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY204245; AAP20640.1; -.  
 DR HSSP; P21859; IJ2L.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:000735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:000729; P:integrin-mediated signaling pathway; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR GO; GO:000508; P:proteinolysis and peptidolysis; IEA.  
 DR Interpro; IPR01762; Disintegrin.  
 DR Interpro; IPR003870; Peptidase\_M12B.  
 DR Interpro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Interpro; IPR001515; Ribosomal\_L32E.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR Pfam; PF01421; Reprolysin; 1.  
 DR Prodom; PD000664; DISIN; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00215; ADAM\_MERRO; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR PROSITE; PS050214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Integrin.  
 SQ SEQUENCE 478 AA; 53443 MW; CD2FBC975F62A771 CRC64;

Query Match 88.7%; Score 339; DB 2; Length 478;  
 Best Local Similarity 84.6%; Pred. No. 2.3e-28;  
 Matches 55; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Oy 1 DAPANCCDAATCKLTGSGCAGDGLCCDOCKFMEGTVCRRGDDYNGISAGCPR 60  
 Db 414 DSGPNCPCDAATCKLRPGAGCAEGGCCQCRFMKEGTVCRRGDDYNGISAGCPR 473

AC Q80124; 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE disintegrin (Fragment).  
 OS Bothrops alternans.  
 EC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidoauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Ovipidae; Crotalinae; Bothrops.  
 RN NCBI\_TaxID=64174;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Ramos O.H.P.; Selistre-de-Araujo H.S.;  
 RA Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL; AY252516; AA075107.1; -.  
 DR HSSP; P21859; 122L.  
 DR GO; GO:0007229; P:integrin-mediated signaling pathway; IBA.  
 DR InterPro; IPR001762; Disintegrin.  
 DR Pfam; PF00200; Disintegrin\_1.  
 DR PRINTS; PRO0289; DISINTEGRIN.  
 DR PRODOM; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN\_1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 KW Integrin.  
 FT NON-TER 1 1  
 SQ SEQUENCE 77 AA; 817.9 MW; 680501C26E7ED496 CRC64;

Query Match 88.0%; Score 336; DB 2; Length 77;  
 Best Local Similarity 87.3%; Pred. No. 9\_9e-29; Mismatches 4; Indels 0; Gaps 0;  
 Matches 55; Conservative 55; Reprolysin; 1.  
 DR InterPro; IPR001762; Disintegrin.  
 DR Pfam; PF00200; Peptidase\_M12B\_N.  
 DR PRODOM; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN\_1.  
 DR PROSITE; PS00427; Disintegrin\_1; 1.  
 DR PROSITE; PS50214; Disintegrin\_2; 1.  
 DR PROSITE; PS50215; ADAM MEROP; 1.  
 DR PROSITE; PS50216; Zinc\_finger\_C2H2.  
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 20  
 FT PROPER 21 191  
 FT CHAIN 192 392  
 FT PROPEP 393 410  
 FT CHAIN 411 484  
 FT PROPER 462 464  
 FT METAL 330 330  
 FT ACT\_SITE 331 331  
 FT METAL 334 334  
 FT METAL 340 340  
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QY  
Db 62 PFHA 65  
70 PLHA 73

Search completed: November 3, 2005, 08:18:51  
Job time: 179 secs

RX MEDLINE=90283343; PubMed=2191722; DOI=10.1016/0167-4838(90)90229-9;  
RA Williams J., Rucinski B., Holt J., Niewarowska S.;  
RT "Elegants J., and alcobalbrin purified peptides from viper venoms:  
RT homologies with the RGDS domain of fibrinogen and von Willebrand  
RT factor.";  
RT

RT RX MEDLINE=9124240; PubMed=2036389; RA Calvete J.J., Schaefer W., Sozzi TA., Lu W., Cook J.J., Jameson B.A., RA Niewiarowski S.; Identification of the disulfide bond pattern in albolabrin, an RGD-containing peptide from the venom of *Trimeresurus albolabris*: RT significance for the expression of platelet aggregation inhibitory RT activity.";

RP 137  
STRUCTURE BY NMR.  
RX MEDLINE=94109384; PubMed=8281937;  
RA Jaseba M., Smith K.J., Lu X., Williams J.A., Trayer H., Trayer I.P.,  
RA Hyde E. I.,  
RT "1H-NMR studies and secondary structure of the RGD-containing snake  
RT toxin, albolabrin.;"  
RL Bur. J. Biochem. 218:853-860(1993).  
RN [4]  
RN

Smith K.J., Jaseja M., Lu X., Williams J.A., Hyde E.I., Trayer I.P.;  
 "Three-dimensional structure of the RGK-containing snake toxin  
 allobabrin in solution, based on <sup>1</sup>H NMR spectroscopy and simulated  
 annealing calculations.";  
 J. Pept. Protein Res. 48:220-228 (1996).  
 -i- FUNCTION: Inhibits fibrinogen interaction with platelet receptors  
 expressed on glycoprotein IIb-IIIa complex. Acts by binding to the

CC inhibits aggregation induced by ADP, thrombin, platelet-activating factor and collagen.  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC SIMILARITY: Belongs to the integrin family.

CC -- TISSUE SPECIFICITY: Expressed by the venom gland  
 CC -- SIMILARITY: Belongs to the disintegrin family.  
 DR PIR; A23731; A23731.

BR HESSP; BL 8919; LNU: Digitized by srujanika@gmail.com

DR InterPro; IPR001762; Disintegrin.  
DR Pfam; PF00200; Disintegrin; 1.  
DR PRINTS; PR00289; DISINTEGRIN.

FT BLOOD COAGULATION: Cell adhesion, direct protein sequencing, platelet-DTS/EDTA 6 15 Probable

FT  
DISULFID  
8  
16  
Probable.

FT DISULFID 21 35 Probable.

FT DISULFID 47 66 Cell attachment site.  
FT SITE 51 53  
SO SEQUENCE 73 AA: 7573 MW: F7E0112E246F8B14 CRC64:

Query Match 87.4%; Score 334; DB 1; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.5e-28;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0;  
 Gaps 0;

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2	APANPCDAATQKLTGTSQCADGLCCDOCKENPKEGIVCRRARGDDDDYCNGISAGCPRN 61
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:SEQ ID NO:21: LENGTH: 72  
; 5182260-21

Query Match Best Local Similarity 88.2%; Score 337; DB 6; Length 72;  
; Matches 55; Conservative 87.3%; Pred. No. 1.6e-26; Indels 0; Gaps 0;  
; SEQ 2 APANPCCDAATCKLUTGSGQCADGLCCDQCKMKGTVCRARGDDIDDYCNNGISAGCPRN 61  
; Db 10 SPENPCCDAATCKLURGAGQCAEGLCCDQCKMKGTVCRARGDDVDNYCNNGISAGCPRN 69

RESULT 3  
5182260-21  
; Patent No. 5182260  
; APPLICANT: MARAGANOBE, JOHN M.; JAKUBOWSKI, JOSEPH A.  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM  
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING  
; THOSE INHIBITORS AND COMPOSITIONS USING THEM  
; NUMBER OF SEQUENCES: 22  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,313  
; FILING DATE: 01-NOV-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 303,585  
; FILING DATE: 27-JAN-1989  
; SEQ ID NO:21:  
; LENGTH: 72

Query Match Best Local Similarity 88.2%; Score 337; DB 6; Length 72;  
; Matches 55; Conservative 87.3%; Pred. No. 1.6e-26; Indels 0; Gaps 0;  
; SEQ 2 APANPCCDAATCKLUTGSGQCADGLCCDQCKMKGTVCRARGDDIDDYCNNGISAGCPRN 61  
; Db 10 SPENPCCDAATCKLURGAGQCAEGLCCDQCKMKGTVCRARGDDVDNYCNNGISAGCPRN 69

RESULT 4  
5182260-2  
; Patent No. 5182260  
; APPLICANT: MARAGANOBE, JOHN M.; JAKUBOWSKI, JOSEPH A.  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM  
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING  
; THOSE INHIBITORS AND COMPOSITIONS USING THEM  
; NUMBER OF SEQUENCES: 22  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,313  
; FILING DATE: 01-NOV-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 303,585  
; FILING DATE: 27-JAN-1989  
; SEQ ID NO:2:  
; LENGTH: 73

Query Match Best Local Similarity 88.2%; Score 337; DB 6; Length 73;  
; Matches 55; Conservative 87.3%; Pred. No. 1.6e-26; Indels 0; Gaps 0;  
; SEQ 2 APANPCCDAATCKLUTGSGQCADGLCCDQCKMKGTVCRARGDDIDDYCNNGISAGCPRN 61  
; Db 11 SPENPCCDAATCKLURGAGQCAEGLCCDQCKMKGTVCRARGDDVDNYCNNGISAGCPRN 70

RESULT 5  
5182260-2  
; Patent No. 5182260  
; APPLICANT: MARAGANOBE, JOHN M.; JAKUBOWSKI, JOSEPH A.  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM  
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING  
; THOSE INHIBITORS AND COMPOSITIONS USING THEM  
; NUMBER OF SEQUENCES: 22  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,313  
; FILING DATE: 01-NOV-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 303,585  
; FILING DATE: 27-JAN-1989  
; SEQ ID NO:2:  
; LENGTH: 73

Query Match Best Local Similarity 88.2%; Score 337; DB 6; Length 73;  
; Matches 55; Conservative 87.3%; Pred. No. 1.6e-26; Indels 0; Gaps 0;  
; SEQ 2 APANPCCDAATCKLUTGSGQCADGLCCDQCKMKGTVCRARGDDIDDYCNNGISAGCPRN 61  
; Db 11 SPENPCCDAATCKLURGAGQCAEGLCCDQCKMKGTVCRARGDDVDNYCNNGISAGCPRN 70

RESULT 6  
US-07-965-674-14  
; Sequence 14, Application US/07965674  
; Patent No. 5380646  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Linda C.  
; TITLE OF INVENTION: Thrombus Detection Using  
; TITLE OF INVENTION: Radiolabelled Disintegrin  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/965, 674  
; FILING DATE: 15921019  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

```

NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE DOCKET NUMBER: 6056-173
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEX: NO. 580646
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-965-674-14

Query Match 87.4%; Score 334; DB 1; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26; Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Unger, Evan C
PATENT NO. 612323
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: No. 65-21211el Sequence
US-08-993-165-15

RESULT 7
Sequence 15, Application US/08993165A
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; PATENT NO. 612323
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: No. 65-21211el Sequence
; US-08-993-165-15

Query Match 87.4%; Score 334; DB 3; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26; Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Wu, Yunqiu
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
US-08-993-165-15

RESULT 8
Sequence 15, Application US/09243640
; GENERAL INFORMATION:
; APPLICANT: Wu, Yunqiu
; PATENT NO. 6521211
; FILE REFERENCE: DUB-0463
; CURRENT APPLICATION NUMBER: US/09/243,640
US-09-243-640-13

Query Match 87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26; Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Unger, Evan C
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
US-09-243-640-13

RESULT 9
Sequence 15, Application US/08928847
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; FILE REFERENCE: BMS0411
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-15

Query Match 87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26; Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Wu, Yunqiu
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
FEATURE:
OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-15

RESULT 10
Sequence 9, Application US/09460295B
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; PATENT NO. 6710030
; FILE REFERENCE: DUB-0463
; CURRENT APPLICATION NUMBER: US/09/243,640
US-09-243-640-13

Query Match 87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26; Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
FILE REFERENCE: DUB-0463
CURRENT APPLICATION NUMBER: US/09/243,640
US-09-243-640-13

RESULT 11
Sequence 9, Application US/09460295B
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; PATENT NO. 6710030
; FILE REFERENCE: DUB-0463
; CURRENT APPLICATION NUMBER: US/09/243,640
US-09-243-640-13

Query Match 87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26; Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
FILE REFERENCE: DUB-0463
CURRENT APPLICATION NUMBER: US/09/243,640
US-09-243-640-13

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TITLE OF INVENTION: CONTOURNOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS  
 TITLE OF INVENTION: OTHER CONDITIONS  
 FILE REFERENCE: 1279-319C3/09801388  
 CURRENT APPLICATION NUMBER: US/09/460, 295B  
 CURRENT FILING DATE: 1999-12-10  
 PRIOR APPLICATION NUMBER: US 09/163, 047  
 PRIOR FILING DATE: 1998-09-29  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO: 9  
 LENGTH: 73  
 TYPE: PRT  
 ORGANISM: Trimeresurus albolabris  
 US-09-460-295B-9

Query Match 87.4%; Score 334; DB 4; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 3.2e-26; 5; Mismatches 5; Indels 0; Gaps 0;  
 Matches 54; Conservative

Qy 2 APANPCDAATCKLUTGSQCAGLGLCQCKMKGTVCRARGDDDDYCNGISAGCPRN 61  
 Db 10 SPANPCDAATCKLKLPGAQCCRGGLCDQCSFMKKGTCRARGDDDDYCNGISAGCPRN 69

Qy 62 PFHA 65  
 Db 70 PLHA 73

RESULT 11

US-09-813-484-15  
 Sequence 15, Application US/09813484  
 PATENT NO. 6716412  
 GENERAL INFORMATION:  
 APPLICANT: Unger, Evan C.  
 TITLE OF INVENTION: 6716412| Methods of Ultrasound Treatment Using Gas Or Gaseous Title of Invention: Filled Compositions  
 FILE REFERENCE: UNGR600  
 CURRENT APPLICATION NUMBER: US/09/813, 484  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 08/929, 847  
 PRIOR FILING DATE: 1997-09-15  
 NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: Patentin version 3.1  
 LENGTH: 73  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Completely synthetic sequence  
 US-09-813-484-15

Query Match 87.4%; Score 334; DB 4; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 3.2e-26; 5; Mismatches 5; Indels 0; Gaps 0;  
 Matches 54; Conservative

Qy 2 APANPCDAATCKLUTGSQCAGLGLCQCKMKGTVCRARGDDDDYCNGISAGCPRN 61  
 Db 10 SPANPCDAATCKLKLPGAQCCRGGLCDQCSFMKKGTCRARGDDDDYCNGISAGCPRN 69

Qy 62 PFHA 65  
 Db 70 PLHA 73

RESULT 12

US-09-776-268A-1  
 Sequence 1, Application US/09776268A  
 PATENT NO. 6537551  
 GENERAL INFORMATION:  
 APPLICANT: KIM, Doo-Sik  
 APPLICANT: CHUNG, Kuang Hoe  
 APPLICANT: KANG, In-Cheol  
 TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT  
 FILE REFERENCE: 0136/1F73-US1  
 CURRENT APPLICATION NUMBER: US/09/0776, 268A  
 CURRENT FILING DATE: 2002-02-02  
 PRIOR APPLICATION NUMBER: US 09/335, 088  
 PRIOR FILING DATE: 1999-06-17  
 PRIOR APPLICATION NUMBER: KR 99-20579  
 PRIOR FILING DATE: 1999-06-04  
 PRIOR APPLICATION NUMBER: KR 99-23778  
 PRIOR FILING DATE: 1998-06-23  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO: 1  
 LENGTH: 73  
 TYPE: PRT

Sequence 14, Application PC/US9309523  
 GENERAL INFORMATION:  
 APPLICANT: Temple University - Of The Commonwealth  
 APPLICANT: System of Higher Education  
 APPLICANT: Knight, Linda C. and  
 APPLICANT: Maurer, Alan H.  
 TITLE OF INVENTION: Thrombus Detection Using

; ORGANISM: Agkistrodon halys brevicaudus  
; US-09-776-268A-1

Query Match 86.9%; Score 332; DB 4; Length 73;  
Best Local Similarity 84.4%; Pred. No. 5.1e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Db 10 SPGNPCDAATCKLURGQACGICLQCDQCKMKEGTICRRARGDDDDYCGISAGCPRN 69  
Qy 62 PPFA 65  
Db 70 PLHA 73

RESULT 14  
US-09-540-448-15

; Sequence 15, Application US/09540448  
; Patent No. 6403056

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Charged Lipids and Uses For The Same

FILE REFERENCE: UGR1592

CURRENT APPLICATION NUMBER: US/09/540, 448

CURRENT FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 08/925, 353

PRIOR FILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence  
US-09-540-448-15

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Best Local Similarity 82.8%; Pred. No. 1e-25;  
Matches 53; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db 10 SPANPCDAATCKLURGQACGICLQCDQCKMKEGTICRRARGDDDDYCGISAGCPRN 69  
Qy 62 PPFA 65  
Db 70 PLHA 73

Search completed: November 3, 2005, 08:20:24  
Job time : 43 secs

US-10-046-001-15

Query Match 86.1%; Score 329; DB 4; Length 73;  
Best Local Similarity 82.8%; Pred. No. 1e-25;  
Matches 53; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLURGQSQCADGLCDQCKMKEGTVCRRARGDDDDYCGISAGCPRN 61  
Db 10 SPANPCDAATCKLURGQACGICLQCDQCKMKEGTICRRARGDDDDYCGISAGCPRN 69  
Qy 62 PPFA 65  
Db 70 PLHA 73

RESULT 15

; Sequence 15, Application US/10046801  
; Patent No. 6408720

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Charged Lipids and Uses For The Same

FILE REFERENCE: UGR1592

CURRENT APPLICATION NUMBER: US/10/046-801

CURRENT FILING DATE: 2002-05-13

PRIOR APPLICATION NUMBER: US/09/540, 448

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 08/925, 353

PRIOR FILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: No. 6408720el Sequence

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Om protein - protein search, using sw model  
Run on: November 3, 2005, 08:14:38 ; Search time 169 Seconds  
(without alignments)  
160.927 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1867879 seqs, 418409474 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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21: /cgn2\_6/prodata/1/pbpa/US60\_NEW\_PUB.pep: \*  
22: /cgn2\_6/prodata/1/pbpa/US60\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID

----- Description -----

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	483	14	US-10-439-332-2 Sequence 2, Appli
2	382	100.0	483	16	US-10-712-584-2 Sequence 2, Appli
3	346	90.6	73	17	US-10-089-473A-10 Sequence 10, Appli
4	345	90.3	73	17	US-10-089-473A-1 Sequence 1, Appli
5	334	87.4	73	9	US-09-813-434-15 Sequence 15, Appli
6	334	87.4	73	14	US-10-439-532-9 Sequence 9, Appli
7	334	87.4	73	16	US-10-712-584-9 Sequence 9, Appli
8	332	86.9	73	9	US-09-776-268A-1 Sequence 1, Appli
9	332	86.1	73	14	US-10-046-011-15 Sequence 15, Appli
10	322	84.3	552	14	US-10-439-532-8 Sequence 8, Appli
11	322	84.3	552	16	US-10-712-584-8 Sequence 8, Appli

Result No.	Score	Query Match	Length	DB ID	Description
1	321.5	84.2	71	10	US-09-832-501-37 Sequence 37, Appli
13	321.5	84.2	71	14	US-10-439-532-7 Sequence 7, Appli
14	321.5	84.2	71	16	US-10-712-584-7 Sequence 2, Appli
15	286	74.9	478	14	US-10-078-866-2 Sequence 10, Appli
16	266	69.6	73	14	US-10-439-532-10 Sequence 14, Appli
17	266	69.6	73	16	US-10-712-584-10 Sequence 23, Appli
18	265	69.4	111	9	US-09-921-823-23 Sequence 8, Appli
19	265	69.4	195	9	US-09-921-823-8 Sequence 6, Appli
20	261	68.3	71	15	US-10-381-588A-6 Sequence 2, Appli
21	261	68.3	463	15	US-10-383-588A-2 Sequence 8, Appli
22	261	68.3	481	15	US-10-383-588A-8 Sequence 10, Appli
23	258	67.5	69	9	US-09-813-484-14 Sequence 14, Appli
24	244	63.9	70	9	US-09-813-484-17 Sequence 17, Appli
25	244	63.9	70	14	US-10-046-801-17 Sequence 17, Appli
26	243	63.6	70	10	US-09-961-656-9 Sequence 9, Appli
27	241.5	63.2	70	10	US-09-813-484-16 Sequence 16, Appli
28	238.5	62.4	68	9	US-09-813-484-16 Sequence 16, Appli
29	238.5	62.4	68	14	US-10-046-801-16 Sequence 11, Appli
30	228	59.7	68	14	US-10-439-532-11 Sequence 11, Appli
31	228	59.7	68	16	US-10-712-584-11 Sequence 11, Appli
32	228	59.7	478	14	US-10-439-532-14 Sequence 12, Appli
33	228	59.7	478	16	US-10-712-584-14 Sequence 12, Appli
34	223	58.4	9	US-09-921-823-2 Sequence 13, Appli	
35	219	57.3	611	9	US-09-921-823-17 Sequence 13, Appli
36	214	56.0	616	18	US-10-482-925A-1 Sequence 14, Appli
37	207.5	54.3	76	10	US-09-877-843-88 Sequence 14, Appli
38	199	52.1	606	14	US-10-439-532-12 Sequence 15, Appli
39	199	52.1	606	16	US-10-712-584-12 Sequence 15, Appli
40	197	51.6	282	9	US-09-840-977-109 Sequence 16, Appli
41	195.5	51.2	571	14	US-10-439-532-13 Sequence 17, Appli
42	195.5	51.2	571	16	US-10-712-584-13 Sequence 17, Appli
43	191	50.0	49	9	US-09-840-977-8 Sequence 18, Appli
44	191	50.0	49	9	US-09-840-977-8 Sequence 18, Appli
45	191	50.0	49	20	US-11-066-697-1132 Sequence 1132, Ap

#### ALIGNMENTS

RESULT 1  
US-10-439-532-2

; Sequence 1, Application US/10439532  
; Publication No. US20030186884A1

; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
; TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS  
; TITLE OF INVENTION: OTHER CONDITIONS  
; FILE REFERENCE: 1279-038N2, 9891388

; CURRENT APPLICATION NUMBER: US10-439, 532

; CURRENT FILING DATE: 2003-05-16

; PRIOR APPLICATION NUMBER: US09/591, 552

; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 483

; TYPE: PRT

; ORGANISM: Agkistrodon contortrix

US-10-439-532-2

Query Match	Length	DB ID	Description
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Matches	65	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	419	DAPANPCDAATCKLTTGSQCADGICGCCDCKFMEKGTVRRARGDDYYCNGISAGCP	478
Qy	61	NPFHA 65	
Db	479	NPFHA 483	





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; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925, 353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1el Sequence
; US-10-046-801-15

Query Match 86.1%; Score 329; DB 14; Length 73;
Best Local Similarity 82.8%; Pred. No. 4.2e-27; Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS
; FILE REFERENCE: 1279-338N2/19801388
; CURRENT APPLICATION NUMBER: US/10/439, 532
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US09/591, 552
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 8
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Trimeresurus gramineus
; US-10-439-532-B

RESULT 10
US-10-439-532-B Application US/10439532
; Sequence 8 Application US/10439532
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS
; FILE REFERENCE: 1279-338N2/19801388
; CURRENT APPLICATION NUMBER: US/10/439, 532
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US09/591, 552
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 8
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Trimeresurus gramineus
; US-10-712-584-B

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; Publication No. US20030199043A1
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J.
; APPLICANT: Sleep, Darrell
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; APPLICANT: Prior, Christopher P.
; APPLICANT: Sadeghi, Homa
; TITLE OF INVENTION: Albumin Fusion Proteins
; CURRENT APPLICATION NUMBER: US/09/832, 501
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 37
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
; US-09-832-501-37

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; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Ritter, Matthew
; TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712, 584
; CURRENT FILING DATE: 2003-11-12
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
; US-09-832-501-37

Query Match 84.2%; Score 321.5; DB 10; Length 71;
Best Local Similarity 84.2%; Pred. No. 2.5e-26; Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Ritter, Matthew
; TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712, 584
; CURRENT FILING DATE: 2003-11-12
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
; US-09-832-501-37

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Db          69 PFH 71
; Best Local Similarity 85.7%; Pred. No. 2.5e-26; Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
; Sequence 7, Application US/10439532
; Publication No. US200301868841
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS
; FILE REFERENCE: 1279-33RN2/02801388
; CURRENT APPLICATION NUMBER: US/10/439,532
; CURRENT FILING DATE: 2003-05-16
; PRIORITY NUMBER: US09/591,552
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
; US-10-439-532-7

Query Match          84.2%; Score 321.5; DB 14; Length 71;
Best Local Similarity 85.7%; Pred. No. 2.5e-26;
Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
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; Best Local Similarity 73.4%; Pred. No. 7.3e-22;
; Sequence 2, Application US/10078866
; Publication No. US200300963931
; GENERAL INFORMATION:
; APPLICANT: FOX, BRIAN A.
; APPLICANT: SHEPPARD, PAUL O.
; TITLE OF INVENTION: Disintegrin Homolog, zenk16
; FILE REFERENCE: 01-05
; CURRENT APPLICATION NUMBER: US/10/078,866
; CURRENT FILING DATE: 2002-02-20
; PRIORITY NUMBER: 60/270,276
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
; US-10-078-866-2

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; Search completed: November 3, 2005, 08:23:19
; Job time : 171 secs
; Prior Application Number: US 08/540,423
; Current Filing Date: 2003-11-12
; Prior Application Number: US09/591,552
; Prior Filing Date: 2000-06-08
; Prior Application Number: US 08/141,321
; Prior Filing Date: 1993-10-22
; Prior Application Number: US 08/540,423
; Prior Filing Date: 1995-10-10
; Prior Application Number: US 08/632,691
; Prior Filing Date: 1996-04-15
; Prior Application Number: US 08/745,603
; Prior Filing Date: 1996-11-08
; Prior Application Number: US 09/163,047
; Prior Filing Date: 1998-09-29
; Prior Application Number: US09/460,295
; Prior Filing Date: 1999-12-10
; Number of Seq Id Nos: 15
; Software: PatentIn version 3.1
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; Length: 71
; Type: PRT
; Organism: Agkistrodon piscivorus
; US-10-712-584-7

Query Match          84.2%; Score 321.5; DB 16; Length 71;

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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